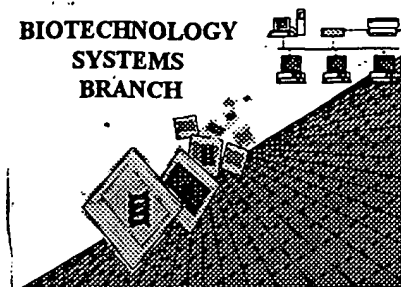


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/831,253
Source: P45/09
Date Processed by STIC: 12/19/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202

Or

- U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, Virginia 22202

4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/831,253

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
 Wrapped Aminos
 The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☒ Invalid Line Length
 The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
 Numbering
 The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
 The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
 Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
 "bug"
 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
 (OLD RULES)
 Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
 (NEW RULES)
 Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ☐ Use of n's or Xaa's
 (NEW RULES)
 Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
 Response
 Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
 Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
 "bug"
 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
 n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,253

DATE: 12/19/2001

TIME: 16:03:12

Input Set : A:\831253seq.nov.txt

Output Set: N:\CRF3\12192001\I831253.raw

3 <110> APPLICANT: EZQUERRO SAENZ, Ignacio Jose
 4 LASARTE SAGASTIBELZA, Juan Jose
 5 PRIETO VALTUENA, Jesus
 6 BORRAS CUESTA, Francisco
 8 <120> TITLE OF INVENTION: TGFbb1-inhibitor peptides
 10 <130> FILE REFERENCE: U-013446-9
 12 <140> CURRENT APPLICATION NUMBER: 09/831,253
 C--> 13 <141> CURRENT FILING DATE: 2001-11-20
 15 <150> PRIOR APPLICATION NUMBER: PCT/ES99/00375
 16 <151> PRIOR FILING DATE: 1999-11-23
 18 <150> PRIOR APPLICATION NUMBER: P9802465
 19 <151> PRIOR FILING DATE: 1998-11-24
 21 <160> NUMBER OF SEQ ID NOS: 10

Please
consult Sequence
Rules for valid
format
 Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

E--> 24 <210> SEQ ID NO: SEQ ID NO: 1
 26 <211> LENGTH: 15
 E--> 28 <212> TYPE: Peptide
 30 <213> ORGANISM: Artificial sequence
 W--> 32 <220> FEATURE: Domain
 34 <223> OTHER INFORMATION: Derived from TGFbb1, position 319-333
 E--> 36 <400> SEQUENCE: His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu
 37 5 10 15
 E--> 40 <210> SEQ ID NO: SEQ ID NO: 2
 42 <211> LENGTH: 14
 E--> 44 <212> TYPE: Peptide
 46 <213> ORGANISM: Artificial sequence
 W--> 48 <220> FEATURE: Domain
 50 <223> OTHER INFORMATION: Derived from TGFbb1, position 322-335
 E--> 52 <400> SEQUENCE: Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
 53 5 10
 E--> 56 <210> SEQ ID NO: SEQ ID NO: 3
 58 <211> LENGTH: 12
 E--> 60 <212> TYPE: Peptide
 62 <213> ORGANISM: Artificial sequence
 W--> 64 <220> FEATURE: Domain
 66 <223> OTHER INFORMATION: Deduced as complementary to TGFbb1, position 731-742
 E--> 68 <400> SEQUENCE: Thr Ser Leu Asp Ala Thr Met Ile Trp Thr Met Met
 69 5 10
 E--> 72 <210> SEQ ID NO: SEQ ID NO: 4
 74 <211> LENGTH: 15
 E--> 76 <212> TYPE: Peptide
 78 <213> ORGANISM: Artificial sequence
 W--> 80 <220> FEATURE: Domain
 82 <223> OTHER INFORMATION: Overlapping with the extracellular region of the rat type III receptor,

All following
pages

<210> ~~SEO ID NO:~~ 3

<211> 12

<212> Peptide

<213> Artificial sequence

<220> Domain

<223> Deduced as complementary to TGFbb1, position 731-742

4007 3

<400> Thr Ser Leu Asp Ala Thr Met Ile Trp Thr Met Met
5 10

<210> SEQ ID NO: 4

<211> 15

<212> Peptide

<213> Artificial sequence

<220> Domain

<223> Overlapping with the extracellular region of the rat type III receptor,
position 245-259

4007 4

<400> Ser Asn Pro Tyr Ser Ala Phe Gln Val Asp Ile Ile Val Asp Ile
5 10 15

<210> SEQ ID NO: 5

<211> 9

<212> Peptide

<213> Artificial sequence

<220> Domain

<223> Modification P54 deduced as complementary to TGFbb1, position 731-742

4007 5

<400> Thr Ser Leu Met Ile Trp Thr Met Met
5

<210> SEQ ID NO: 6

<211> 14

<212> Peptide

<213> Artificial sequence

<220> Domain

<223> Derived from the modified human type III receptor, position 729-742

~~(400)~~ 6

<400> Thr Ser Leu Asp Ala Ser Ile Ile Trp Ala Met Met Gln Asn
5 10

<210> ~~SEQ ID NO:~~ 7

<211> 14

<212> Peptide

<213> Artificial sequence

<220> ~~Domain~~

<223> Derived from the modified human type III receptor, position 241-254

<400> Ser Asn Pro Tyr Ser Ala Phe Gln Val Asp Ile Thr Ile Asp
5 10

<210> ~~SEQ ID NO:~~ 8

<211> 15

<212> Peptide

<213> Artificial sequence

<220> ~~Domain~~

<223> Position 247-261 of endoglin

~~(400)~~ 8

<400> Glu Ala Val Leu Ile Leu Gln Gly Pro Pro Tyr Val Ser Trp Leu
5 10 15

<210> ~~SEQ ID NO:~~ 9

<211> 15

<212> Peptide

<213> Artificial sequence

<220> ~~Domain~~

<223> Position 445-459 of endoglin

~~(400)~~ 9

<400> Leu Asp Ser Leu Ser Phe Gln Leu Gly Leu Tyr Leu Ser Pro His
5 10 15

<210> ~~SEQ ID NO:~~ 10

<211> 23

← see
item 2
on Error
summary
sheet

← item 2

<212>(Peptide)

<213> Artificial sequence

<220> Domain

<223> Modification P12, position 322-335 of TGFbb1

2400710

6400710

~~<400>~~ His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 5 10 15

Ile Trp Ser Leu Asp Thr

20

↓ insert a hard return

Per 1.822 of
Sequence
Rule, a
MAXIMUM
of 16
amino acids
per line